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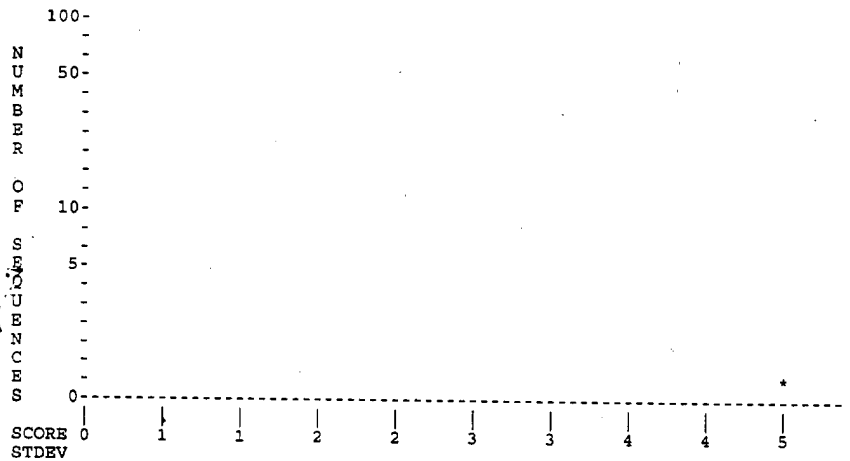
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-963-896-1.res made by bshears on Tue 20 Jan 104 11:54:26-PST.

Query sequence being compared:US-09-963-896-1 (1-141)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-963-896-1 (1-141) with:
File : /home/bshears/harris*.pep



PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	5	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues: 410
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-963-896-2-	Sequence 2, Application U	410	5	26	0.00	0

1. US-09-963-896-1 (1-141)
US-09-963-896-2- Sequence 2, Application US/09963896

Sequence 2, Application US/09963896
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/963,896
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTTUT03
CLONE: 1999442
SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Initial Score = 5 Optimized Score = 26 Significance = 0.00
Residue Identity = 20% Matches = 33 Mismatches = 105
Gaps = 21 Conservative Substitutions = 0

```
X       10          20          30          40          50          60
MVHVAYSLCLPMR---RSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY-ISFGIMSLGLLSLLAVTSI--
MFLPPVVLAIRSRYVLEAAVYTFTMFFSTFYHA---CDQPGIVVFCIMDYDVLQFCDFLGSLMSVWVTVIAM
X       10          20          30          40          50          60

      70          80          90          100         110         120
----PSVSNALNWREFSFIQSTL-----GYVALL-ISTFHVLIYGWKRAFEEEYYRFYTPP--NFVLALVLP
ARLQPVVKQVLYLLGAMLLSMALQLDRHGLWNLLGPSLFALGILATAWTVRSVRRRHCYPPTWRRWLFYLCP
70          80          90          100         110         120         130         140

 130       140
SIVILDLLQLCRYPD
GSLIAGSAVLLYAFVETRDNYFYIHSIWHMLIAGSVGFLLPPRAKTDHGVPSGARARGCGYQLCI
```